Application No. 10/087,541
Amendment dated September 18, 2007
Response to Office Action dated June 18, 2007

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1.   (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:

(a)   constructing an index table, said index table comprising a plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields, said constructing step comprising the steps of:

      (i)   selecting a first peptide from said plurality of database peptides;

      (ii)   calculating a plurality of associated masses for said first peptide;

      (iii)   selecting a first associated mass from said plurality of associated masses;

      (iv)   referencing a first record from said plurality of records, said first record corresponding to said first associated mass;

      (v)   entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;

      (vi)   repeating steps (iii)-(v) for at least one other associated mass from said plurality of associated masses;

      (vii)   repeating steps (i)-(vi) for at least one other peptide from said plurality of database peptides; and

(b)   generating a plurality of comparison scores, said plurality of comparison scores

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corresponding to said plurality of database peptides, said generating step comprising the steps of:

    (i)   generating a plurality of query mass values for said query peptide;

    (ii)   selecting a first query mass value from said plurality of query mass values;

    (iii)   referencing a second record from said plurality of records, said second record corresponding to said first query mass value;

    (iv)   selecting a second field from said second record, said second field comprising a second peptide index;

    (v)   selecting a first comparison score from said plurality of comparison scores, said first comparison score corresponding to said second peptide index;

    (vi)   incrementing said first comparison score;

    (vii)   repeating steps (ii)-(vi) for at least one other query mass value selected from said plurality of query mass values.

2.   (Withdrawn) The method of claim 1 wherein said generating step (b)(i) comprises the step of performing mass spectroscopy on said query peptide.

3.   (Withdrawn) The method of claim 2 wherein said mass spectroscopy is performed by a method selected from the set consisting of: Fourier transform ion cyclotron resonance ("FTICR"), quadrupole mass spectroscopy, ion trap mass spectroscopy, and time-of-flight mass spectroscopy.

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4.   (Withdrawn) The method of claim 1 wherein said calculating step (a)(ii) comprises the step of calculating a plurality of associated masses for said first peptide, said plurality of associate masses comprising a plurality of primary masses and a plurality of complementary masses.

5.   (Withdrawn) The method of claim 1 wherein said generating step (b) further comprises the step of multiplying said first comparison score by a weight value, wherein said weight value is a function of the type of mass value.

6.   (Withdrawn) The method of claim 5 wherein said type of mass value is selected from the group consisting of: y-ion, b-ion, peak mass, and complementary mass.

7.   (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:

        (a)   constructing a first index table, said first index table comprising a first plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields; and

        (b)   constructing a second index table, said second index table comprising a second plurality of records corresponding to said plurality of allowed mass values, said records comprising zero or more fields; and

        (c)   calculating a plurality weight values, said weight values set according to the

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predictive value of said first and second index tables.

8.   (Currently amended) A method for peptide modification evaluation comprising the steps

of:

        a) identifying a fragmentation spectrum for a sample containing at least one modified

query peptide, the at least one modified query peptide having a mass, at least a portion of which

is attributable to a modification associated with the at least one modified query peptide, wherein

the fragmentation spectrum is obtained by mass spectrometry and at least a portion of the

fragmentation spectrum comprises mass/charge ratios associated with fragments of the at least

one modified query peptide that are distributed over a spectral range ranging from zero to an

unmodified mass associated with modified query peptide;

        b) apportioning said spectral range for the at least one modified query peptide into a

plurality of mass intervals;

        c) distributing the mass ratios for the fragments of the at least one modified query peptide

over one or more of the plurality of mass intervals;

        d) postulating that a modification of one or more fragments within a mass interval has

occurred resulting in a modified mass ratio for the one or more fragments;

        e) excluding or adjusting modified mass ratios in the mass interval that correspond to at

least one predetermined ion type of the fragments;

        f) comparing the modified mass ratio for the one or more remaining fragments with mass

ratios for fragments associated with at least one known peptide fragmentation spectrum adjusted

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to account for the modification in the mass interval;

g) scoring the mass ratio comparisons between the one or more remaining fragments of

the at least one modified query peptide versus the at least one known peptide fragmentation

spectrum within each the mass interval;

h) repeating steps (d) through (g) for each remaining mass interval of the one or more

mass intervals over which mass ratios are distributed in step (c) to generate respective scored

mass comparisons for each remaining mass interval;

i) summing the scored mass ratio comparison over the plurality of mass intervals

comparisons generated in steps (g) and (h) to generate a summed score for the at least one known

peptide fragmentation spectrum over the spectral range; and

j) identifying at least one known peptide best matching the at least one modified query

peptide when taking the mass of the modification into account, based on the summed score.

9.   (Previously presented) The method of claim 8 further comprising the step of determining

a difference mass for the modified query peptide as being the difference between the molecular

weight of the modified query peptide and the molecular weight of the unmodified query peptide

and further excluding from the analysis fragments associated with the modified query peptide

where the difference mass is not known.

10.   (Previously presented) The method of claim 8 further comprising the step of determining

a difference mass for the modified query peptide as being the difference between the molecular

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weight of the modified query peptide and the molecular weight of the unmodified query peptide

and further adjusting mass ratios for fragments associated with the modified query peptide prior

to the comparison with fragments associated with known peptide fragmentation spectrum.

11.   (Withdrawn) A method for comparing a query peptide to a plurality of database peptides

comprising the step of constructing an index table, said index table comprising a plurality of

records corresponding to a plurality of allowed mass values, said records comprising zero or

more fields, said constructing step comprising the steps of:

(i)   selecting a first peptide from said plurality of database peptides;

(ii)   identifying a modification site on said first peptide;

(iii)   applying a modification to said modification site, producing a first modified

peptide;

(iv)   calculating a plurality of associated masses for said first modified peptide;

(v)   selecting a first associated mass from said plurality of associated masses;

(vi)   referencing a first record from said plurality of records, said first record

corresponding to said first associated mass;

(vii)   entering a first field into said first record, said first field comprising a first peptide

index referencing said first peptide;

(viii) repeating steps (v)-(vii) for at least one other associated mass from said plurality

of associated masses;

(ix)   repeating steps (i)-(viii) for at least one other peptide from said plurality of

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database peptides.

12. (Previously presented) The method of claim 8 wherein the modified query peptide possesses a modification site selected from the group consisting of:

a phosphorylation site,

an oxidation site,

and a substitution site.

13. (Original) The method of claim 12 wherein said phosphorylation site comprises an amino acid selected from the group consisting of: serine, threonine, and tyrosine.

14. (Original) The method of claim 12 wherein said oxidation site comprises an amino acid selected from the group consisting of: cysteine and methionine.

15. (Original) The method of claim 12 wherein said substitution site comprises an amino acid selected from the group consisting of: glutamine, glutamate, asparagine, and aspartate.

16. (Canceled)

17. (Previously presented) The method of claim 8, wherein comparing the modified mass ratio for the one or more fragments of the modified query peptide and the mass ratios for the

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fragments associated with known peptide fragmentation spectrum further identifies modified fragments of the modified query peptide that reside within the mass interval.

18. (Canceled)

19. (Previously presented) The method of claim 8 further comprising collectively evaluating the mass ratio comparisons between the modified query peptide and known peptides to determine a putative identity of the modified query peptide by determining the closest match between the modified query peptide and the known peptides when taking the mass of the modification into account.

20. (Previously presented) The method of claim 8, wherein the at least one predetermined ion type comprises at least one of a b-ion and a y-ion.

21. (Previously presented) The method of claim 20, wherein the at least one predetermined ion type comprises a b-ion.

22. (Previously presented) The method of claim 21, wherein the b-ion comprises a fragment for which charge is retained on the N-terminal cleavage fragment.

23. (Previously presented) The method of claim 21, wherein the excluding or adjusting

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comprises excluding or adjusting any modified mass ratios corresponding to a fragment whose mass ratio is greater than an upper bound of the mass interval.

24.   (Previously presented) The method of claim 20, wherein the at least one predetermined ion type comprises a y-ion.

25.   (Previously presented) The method of claim 24, wherein the y-ion comprises a fragment for which charge is retained on the C-terminal cleavage fragment.

26.   (Previously presented) The method of claim 25, wherein the excluding or adjusting comprises excluding or adjusting any modified mass ratios corresponding to a fragment whose mass ratio is greater than a quantity equal to (two times the mass of a hydrogen atom minus a lower bound of the mass interval).

27.   (Previously presented) The method of claim 8, wherein the modification of the one or more fragments within the mass interval comprises two or more modifications.